

# SEQUENCE LISTING

<110> BOUGUELERET; Lydie  
CUSIN; Isabelle

<120> SECRETED POLYPEPTIDE SPECIES ASSOCIATED  
WITH CARDIOVASCULAR DISORDERS

<130> DV/4-33628A/GEP US-P

<140> 10/561,292

<141> 2005-12-20

<150> 60/484,153

<151> 2003-06-30

<150> PCT/EP2004/007047

<151> 2004-06-29

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 456

<212> PRT

<213> Homo sapiens

<220>

<221> PROPEP

<222> (1)...(456)

<223> Precursor protein of CP22

<400> 1

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          20           25           30
Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr
          35           40           45
Gly Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys
          50           55           60
Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His
65           70           75           80
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys
          85           90           95
Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys
          100          105          110
Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro
          115          120          125
Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro
          130          135          140
Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro
145           150           155           160
Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Glu Gln

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Cys	Lys	Thr	Glu	Lys	Phe	Leu	Ile	His	Ser	Gln	Gln	Pro	Cys	Pro	Gln			
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Gly	Ala	Pro	Asp	Cys	Gln	Lys	Val	Lys	Val	Met	Tyr	Arg	Met	Ala	His			
65					70					75					80			
Lys	Pro	Val	Tyr	Gln	Val	Lys	Gln	Lys	Val	Leu	Thr	Ser	Leu	Ala	Trp			
				85					90					95				
Arg	Cys	Cys	Pro	Gly	Tyr	Thr	Gly	Pro	Asn	Cys	Glu	His	His	Asp	Ser			
			100					105					110					
Met	Ala	Ile	Pro	Glu	Pro	Ala	Asp	Pro	Gly	Asp	Ser	His	Gln	Glu	Pro			
		115					120					125						
Gln	Asp	Gly	Pro	Val	Ser	Phe	Lys	Pro	Gly	His	Leu	Ala	Ala	Val	Ile			
	130					135					140							
Asn	Glu	Val	Glu	Val	Gln	Gln	Glu	Gln	Gln	Glu	His	Leu	Leu	Gly	Asp			
145					150					155					160			
Leu	Gln	Asn	Asp	Val	His	Arg	Val	Ala	Asp	Ser	Leu	Pro	Gly	Leu	Trp			
			165						170					175				
Lys	Ala	Leu	Pro	Gly	Asn	Leu	Thr	Ala	Ala	Ser	Leu	Ser	Asn	Asp	Val			
			180					185					190					
Lys	Asn	Val	Gly	Arg	Cys	Cys	Glu	Ala	Glu	Ala	Gly	Ala	Gly	Ala	Ala			
	195						200					205						
Ser	Leu	Asn	Ala	Ser	Leu	His	Gly	Leu	His	Asn	Ala	Leu	Phe	Ala	Thr			
	210					215				220								
Gln	Arg	Ser	Leu	Glu	Gln	His	Gln	Arg	Leu	Phe	His	Ser	Leu	Phe	Gly			
225					230					235					240			
Asn	Phe	Gln	Gly	Leu	Met	Glu	Ala	Asn	Val	Ser	Leu	Asp	Leu	Gly	Lys			
			245						250					255				
Leu	Gln	Thr	Met	Leu	Ser	Arg	Lys	Gly	Lys	Lys	Gln	Gln	Lys	Asp	Leu			
			260					265					270					
Glu	Ala	Pro	Arg	Lys	Arg	Asp	Lys	Lys	Glu	Ala	Glu	Pro	Leu	Val	Asp			
	275						280					285						
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Glu	Ala	Gly	Ser	Pro	Val	Ala	Phe	Tyr	Ala	Ser	Phe	Ser	Glu	Gly	Thr			
305					310					315					320			
Ala	Ala	Leu	Gln	Thr	Val	Lys	Phe	Asn	Thr	Thr	Tyr	Ile	Asn	Ile	Gly			
			325						330					335				
Ser	Ser	Tyr	Phe	Pro	Glu	His	Gly	Tyr	Phe	Arg	Ala	Pro	Glu	Arg	Gly			
			340					345					350					
Val	Tyr	Leu	Phe	Ala	Val	Ser	Val	Glu	Phe	Gly	Pro	Gly	Pro	Gly	Thr			
	355						360					365						
Gly	Gln	Leu	Val	Phe	Gly	Gly	His	His	Arg	Thr	Pro	Val	Cys	Thr	Thr			
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385					390					395					400			
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Thr

<210> 3  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)...(152)  
 <223> Cardiovascular disorder Plasma Polypeptide 22 (CPP  
 22)

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 20 25 30  
 Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn  
 35 40 45  
 Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr  
 50 55 60  
 Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu  
 65 70 75 80  
 Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His  
 85 90 95  
 Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr  
 100 105 110  
 Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu  
 115 120 125  
 Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe  
 130 135 140  
 Gly Gly Phe Leu Met Phe Lys Thr  
 145 150

<210> 4  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)...(24)  
 <223> Tryptic peptides of CPP 22 found by MS-MS mass  
 spectrometry in plasma samples of individuals with  
 coronary artery disease

<400> 4  
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 Phe Ala Met Ala Glu Leu Gln Lys  
 20

<210> 5  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)...(12)  
 <223> Tryptic peptides of CPP 22 found by MS-MS mass

spectrometry in plasma samples of individuals with  
coronary artery disease

<400> 5

Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr Lys  
1 5 10

<210> 6

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)...(14)

<223> Tryptic peptides of CPP 22 found by MS-MS mass  
spectrometry in plasma samples of individuals with  
coronary artery disease

<400> 6

Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys  
1 5 10

<210> 7

<211> 1371

<212> DNA

<213> Homo sapiens

<220>

<221> variation

<222> (1)...(1371)

<223> Splice variant of the Endoglyx-1 gene and  
comprises the cDNA coding sequence for SEQ ID NO:  
1

<400> 7

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tggaaggcag aggctgagga caccggcaag gaccccgtag gacgtaactg gtgcccctac 180
ccaatgtcca agctgggtcac cttactagct ctttgcaaaa cagagaaatt cctcatccac 240
tcgcagcagc cgtgtccgca gggagctcca gactgccaga aagtcaaagt catgtaccgc 300
atggcccaca agccagtgtt ccaggtcaag cagaagggtg tgacctcttt ggcttgagg 360
tgctgccctg gctacacggg cccaactgc gagcaccacg attccatggc aatccctgag 420
cctgcagatc ctggtgacag ccaccaggaa cctcaggatg gaccagtcag cttcaaacct 480
ggccaccttg ctgcagtgat caatgaggtt gaggtgcaac aggaacagca ggaacatctg 540
ctgggagatc tccagaatga tgtgcaccgg gtggcagaca gcctgccagg cctgtggaaa 600
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tgctgcgagg ccgaggccgg ggccggggcc gcctccctca acgcctccct tcacggcctc 720
cacaacgcac tcttcgccac tcagcgcagc ttggagcagc accagcggct cttccacagc 780
ctctttggga acttccaagg gctcatggaa gccaacgtca gcctggacct ggggaagctg 840
cagaccatgc tgagcaggaa agggaagaag cagcagaaag acctggaagc tccccggaag 900
agggacaaga aggaagcggg gcctttggtg gacatacggg tcacagggcc tgtgccaggt 960
gccttgggcg cggcgctctg ggaggcagga tcccctgtgg ccttctatgc cagcttttca 1020
gaagggacgg ctgccctgca gacagtgaag ttcaacacca catacatcaa cattggcagc 1080
agctacttcc ctgaacatgg ctacttccga gcccctgagc gtggtgtcta cctgtttgca 1140
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cggactccag tctgtaccac tgggcagggg agtgggaagca cagcaacggt ctttgccatg 1260
gctgagctgc agaagggtga gcgagtatgg tttgagttaa cccagggatc aataacaaag 1320
agaagcctgt cgggcactgc atttgggggc ttcctgatgt ttaagacctg a 1371

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<210> 8

<211> 417

<212> PRT

<213> Mus musculus

<220>

<221> PEPTIDE

<222> (1)...(417)

<223> Q8K1Z7, a murine homologue of SEQ ID NO:1

<400> 8

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20      25      30
Asn Arg Pro Gly Met Pro Glu Gly Trp Arg Leu Gly Ala Glu Asp Thr
35      40      45
Ser Arg Asp Pro Ile Arg Arg Asn Trp Cys Pro Tyr Gln Lys Ser Arg
50      55      60
Leu Val Thr Phe Val Ala Ala Cys Lys Thr Glu Lys Phe Leu Val His
65      70      75      80
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Gly Val Arg
85      90      95
Val Met Tyr Arg Val Ala Gln Lys Pro Val Tyr Gln Val Gln Gln Lys
100     105     110
Val Leu Ile Ser Val Asp Trp Arg Cys Cys Pro Gly Phe Gln Gly Pro
115     120     125
Asp Cys Gln Asp His Asn Pro Thr Ala Asn Pro Glu Pro Thr Glu Pro
130     135     140
Ser Gly Lys Leu Gln Glu Thr Trp Asp Ser Met Asp Gly Phe Glu Leu
145     150     155     160
Gly His Pro Val Pro Glu Phe Asn Glu Ile Lys Val Pro Gln Glu Gln
165     170     175
Gln Glu Ile Arg Arg Leu Ser Ser Asp Val Lys Gln Ile Gly Gln Cys
180     185     190
Cys Glu Ala Ser Trp Ala Ala Ser Leu Asn Ser Ser Leu Glu Asp Leu
195     200     205
His Ser Met Leu Leu Asp Thr Gln His Gly Leu Arg Gln His Arg Gln
210     215     220
Leu Phe His Asn Leu Phe Gln Asn Phe Gln Gly Leu Val Ala Ser Asn
225     230     235     240
Ile Ser Leu Asp Leu Gly Lys Leu Gln Ala Met Leu Ser Lys Lys Asp
245     250     255
Lys Lys Gln Pro Arg Gly Pro Gly Glu Ser Arg Lys Arg Asp Lys Lys
260     265     270
Gln Val Val Met Ser Thr Asp Ala His Ala Lys Gly Leu Glu Leu Trp
275     280     285
Glu Thr Gly Ser Pro Val Ala Phe Tyr Ala Gly Ser Ser Glu Gly Ala
290     295     300
Thr Ala Leu Gln Met Val Lys Phe Asn Thr Thr Ser Ile Asn Val Gly
305     310     315     320
Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Lys Arg Gly

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[illegible]